

Udder Classification Based On AMS Data

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Abstract

Since April 2023, CRV uses AMS (Automatic Milking System) data to estimate breeding values for udder conformation traits in the Netherlands and Flanders in addition to data from herd classification. AMS data is used to derive traits for udder depth, distance between the front teats, distance between the rear teats and udder balance. Three teat coordinates are determined and stored by the AMS each milking, all given in millimetres: x (measure of the width), y (measure of the length), and z (measure of the depth). Based on these three teat coordinates, the four udder traits can be derived. Traits are derived for first three parities. The heritability for respectively udder depth, distance between the front teats, distance between the rear teats and udder balance in parity 1 is 0.56, 0.60, 0.45 and 0.45. Based on herd classification, heritabilities for udder depth, front teat placement and rear teat placement are respectively 0.39, 0.31 and 0.29. The genetic correlations between these three traits and corresponding heifer traits based on AMS data are respectively 0.98, 0.98 and 0.99. Traits for later parities show comparable heritabilities and genetic correlations. The repeated records lead to an increase of the heritability and reliability compared to udder depth, front teat placement and rear teat placement based on herd classification. Furthermore, the AMS gives more objective results compared to scores given by herd classifiers. The udder conformation traits based on herd classification are still the traits that are published, while udder balance is introduced as new trait. Due to the usage of AMS data, an increase of reliability for bulls breeding values was found ranging between 0.4 and 3.0%. Adding AMS data to the breeding value estimation of udder conformation traits leads to better estimates of the breeding values for existing udder conformation traits by using more information as well as having a breeding value for the new trait udder balance.

Key words: udder conformation, herd classification, AMS data, udder balance

Introduction

In April 2023, 4 805 dairy farms in the Netherlands were milking their cows with an AMS. This is 33% of the total number of dairy farms in the Netherlands. These farms had 9 825 AMS boxes in total, resulting in on average 2 boxes per farm (Stichting KOM, s.d.).

To attach the milkcup to the teats, the AMS should know the position of the teats. The teat positions make it possible to derive udder conformation traits based on information from data stored by the AMS.

By using AMS data, more information on the conformation of the animal is available in

addition to herd classification data. As there are also animals in the AMS data without information from herd classification, more animals can be included in the breeding value estimation for udder conformation.

The data collection is automatic and therefore less time costly compared to herd classification. Dairy farmers can easily indicate via JoinData (JoinData u.a., Wageningen, the Netherlands) if they are willing to share their AMS data with CRV for the breeding value estimation. With their permission, CRV can upload all milkings on a daily basis. The automatic data collection makes the data also available faster compared to classification scores.

Materials and Methods

Data for breeding value estimation

AMS data from more than 1 400 Dutch dairy farms are available for the genetic evaluation. Those farms are all milking their cows with an AMS from Lely (Lely group, Maassluis, the Netherlands).

Each day, almost 400 000 milkings from the previous day are uploaded and added to the database. There is more data from recent years compared to the first year with data, 2014, because the number of farms milking with an AMS keeps growing.

From each milking, the x, y, and z-coordinates are known. The three teat coordinates are all given in millimetres and are illustrated in Figure 1. Based on those coordinates, four udder traits can be derived: udder depth, distance between the front teats, distance between the rear teats and udder balance. Udder depth is the average z-coordinate of the four teats. Distance between the front teats is the difference in x-coordinates of the front teats. Distance between the rear teats is the difference in x-coordinates between the rear teats. Udder balance is the difference in the average z-coordinates of the rear teats and the average z-coordinates of the front teats.

A positive udder balance means a higher rear udder compared to front udder. The opposite is the case if we speak about a negative udder balance.

Higher breeding values indicate a more positive udder balance. A too positive udder balance is not desired, because this can give problems for the AMS when attaching the milkcup to the rear teats. This makes udder balance an optimum trait.

For each cow, the first and every twentieth milking is used for the breeding value estimation to reduce the data size. The first milking is taken to ensure that each cow in the data is also in the breeding value estimation. 33% of the animals in the AMS data has no

information on udder conformation traits from herd classification.

Data from parity 1 to 3, is used. In the April 2023 breeding value estimation, the number of milking was 5 499 248.

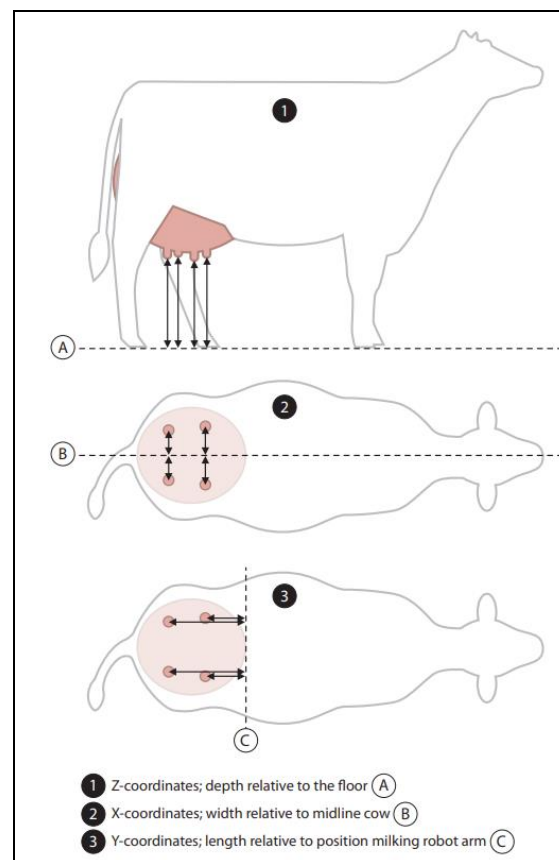


Figure 1. Illustration of teat coordinates.

Parameters

Parameter estimation was based on 868 396 milkings from 89 456 cows with 311 661 milkings belonging to parity 1, 279 191 milking to parity 2 and 277 544 milking to parity 3. All cows were at least 87,5% Holstein. Parameters were estimated using an animal model.

Model

The statistical model used for udder conformation based on AMS data is:

$$Y_{ijklmnopqs} = HYS_i + DIL_j + AFC_k + HY_l + HET_m + REC_n + INB_o + HGT_p + TLE_t + A_q + PME_r + Rest_s$$

In which:

- Y observation on udder conformation on heifers (parity 1), young cows (parity 2) and cows (parity 3);
- HYS herd x year x season x box of milking;
- DIL lactation stadium;
- AFC age of first calving;
- HY herd x year of first calving;
- HET heterosis effect;
- REC recombination effect;
- INB inbreeding effect;
- HGT EBV stature;
- TLE EBV teat length;
- A additive genetic effect;
- PME permanent environmental effect;
- Rest residual term of that which is not explained by the model of Y.

The effects A, PME and Rest are random, the effects HET, REC, INB, HGT and TLE are covariables, the other effects are fixed. Effect AFC is only added to the model for parity 1 and parity 2.

The covariables HGT and TLE are only added to the model for udder depth. Udder depth is based on the z-coordinate, which is measured as the distance from the teat tip to the floor. Stature and teat length of the cow influence this distance, so correction in the model is needed to make udder depth independent from stature and teat length.

Results & Discussion

Udder balance

Udder balance is the average difference in udder depth between rear udder and front udder. The genetic correlations of udder balance with udder conformation traits based on herd type classification are shown in table 1 and are all moderate and positive. This explained the positive trend in phenotype for udder balance over the period 2014 – 2023 as shown in Figure 2. Over this period, udder balance has increased with 5 millimetres for all three parities.

Table 1. Genetic correlation of udder balance parity 1 with udder conformation traits based on herd classification.

trait	genetic correlation
front udder attachment	0.25
front teat placement	0.29
teat length	0.25
udder depth	0.24
rear udder height	0.53
udder support	0.34
rear teat placement	0.36

Table 1 shows that udder balance has the highest genetic correlation (0.54) with rear udder. Because all correlations are moderate, the udder traits based on herd classification cannot give a good prediction of the udder balance of a cow.

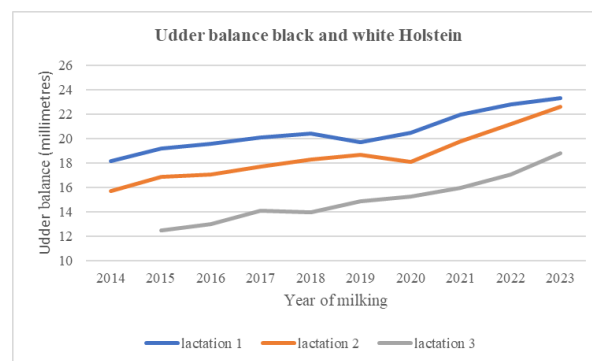


Figure 2. Phenotypic trend in udder balance for black and white Holstein cows in parity 1, parity 2 and parity 3 from 2014 to 2023.

Next to the upward phenotypic trend in udder balance, figure 2 shows that udder balance is most positive in parity 1 and declines over the parities. The decline from parity 1 to parity 2 is about 2 millimetres, from parity 2 to parity 3 the decline is about 3 millimetres.

Genetic parameters

Table 2 shows the heritabilities of the udder conformation traits based on AMS data. Table 3 shows the genetic correlations between similar traits based on herd classification and AMS data for the three different parities. Udder depth from herd classification is

compared to udder depth based on AMS data, and front- and rear teat placement from herd classification are compared to distance between the front- and rear teats based on AMS data. Table 4 shows the genetic correlations between the different parities for the traits based on AMS data.

Table 2. Heritabilities of the traits in parity 1 (p.1), parity 2 (p.2) and parity 3 (p.3).

trait	heritability		
	p.1	p.2	p.3
udder depth	0.56	0.56	0.52
distance front teats	0.60	0.53	0.45
distance rear teats	0.45	0.38	0.33
udder balance	0.45	0.42	0.43

The heritabilities in table 2 are higher compared to the heritabilities for similar traits based on herd classification. Udder depth has a heritability of 0.39, front teat placement has a heritability of 0.31 and rear teat placement has a heritability of 0.29. The increase in heritability by the traits based on AMS data is caused by repeated records of high-quality data.

Table 3. Genetic correlations between similar traits based on herd classification and AMS data for parity 1 (p.1), parity 2 (p.2) and parity 3 (p.3).

trait	genetic correlations		
	p.1	p.2	p.3
udder depth	0.98	0.97	0.97
distance front teats	0.98	0.98	0.97
distance rear teats	0.99	0.99	0.96

The genetic correlations between the traits in table 3 are, independent from parity, close to 1.0, ranging from 0.96 to 0.99. This means that the herd classifiers and AMS measure actually the same trait.

The heritabilities of the udder conformation traits based on AMS data and the genetic correlations with the linear traits from herd classification are comparable with results found in Scandinavia (Rius-Vilarrasa *et al.*, 2016).

Table 4. Genetic correlations for udder traits based on AMS data between parity 1 and 2 (p.1-2), parity 2 and 3 (p.2-3) and parity 1 and 3 (p.1-3).

trait	genetic correlations		
	p.1-2	p.2-3	p.1-3
udder depth	0.97	0.99	0.93
distance front teats	0.99	0.99	0.94
distance rear teats	0.97	0.98	0.90
udder balance	0.96	0.98	0.85

The genetic correlations in table 4 between the different parities are all above 0.90, only udder balance has a lower genetic correlation of 0.85 between parity 1 and 3 which is still considered a high correlation. The different parities give all the same information, therefore parity 1 is used as published trait for udder balance since parity 1 contains the most cows.

Reliabilities

Udder balance in parity 1 is the published trait, the other udder conformation traits based on AMS data are indicator traits. The udder conformation traits based on herd classification profit from the indicator traits using the genetic correlations between the traits because information of extra cows is added, resulting in more reliable breeding values. The increase in reliabilities is shown in table 5.

Table 5. Reliability for udder conformation traits without (old rel.) and with (new rel.) using udder conformation traits based on AMS data as indicator traits and the correlation (corr.) of the bull breeding values between both systems for Holstein bulls born since 2010.

trait	old rel.	new rel.	corr.
front udder attachment	78.1	81.7	0.98
front teat placement	78.7	82.7	0.97
teat length	81.3	81.7	0.99
udder depth	81.4	83.9	0.98
rear udder height	77.1	78.6	0.99
udder support	75.3	79.2	0.97
rear teat placement	77.8	81.8	0.97

The increase in reliability ranges from 0.4 to 4.0%, depending on the covariance structure with the indicator traits. Front udder placement, udder depth and rear teat placement have a relative large increase of respectively 4.0, 2.5 and 4.0%. As shown in table 3, the genetic correlations with the corresponding traits based on AMS data are high, so a relatively large increase in reliability compared to the other traits was also expected.

Conclusions

Teat coordinates from AMS data can be used to derive udder conformation traits. In the Netherlands and Flanders, four udder conformation traits are derived based on AMS data: udder depth, distance between the front teats, distance between the rear teats and udder balance.

Udder balance is a new trait, because it is not scored during the herd classification. Udder balance has a heritability of respectively 0.45, 0.42 and 0.43 for parity 1, parity 2 and parity 3. The genetic correlations with the other udder conformation traits are all moderate positive what causes the upwards trend of 5 millimetres in udder balance over the past ten years.

Repeated records are used for the breeding value estimation, which lead to an increase in heritability and reliability. The heritabilities in parity 1 are 0.56, 0.60 and 0.45 for respectively udder depth, distance between the front teats and distance between the rear teats based on AMS data, while based on herd classification the heritabilities are 0.39, 0.31 and 0.29. Genetic correlations between the traits based on herd classification and AMS data are close to 1.0, ranging from 0.96 to 0.99. Genetic correlations between the different parities for the traits based on AMS data are also close to 1.0, ranging from 0.85 to 0.99.

The use of AMS data in the breeding value estimation for udder conformation lead to an increase of the reliability of the published

udder conformation traits. The increase in reliabilities ranges from 0.4 to 4.0%.

Using AMS data leads to better estimates of the breeding values for udder conformation traits by using more information.

Acknowledgments

AMS data is shared by dairy farmers via JoinData, a Dutch non-profit organization. JoinData is a data platform where farmers are in charge of their own data. Organizations who are willing to use data can only use data from farmers who agree with the use of their data.

The existence of JoinData made is possible for CRV u.a. to make use of AMS data from Dutch dairy herds.

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